

Progress towards x-ray diffraction microscopy of frozen hydrated cells at ALS 9.0.1

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The method of x-ray diffraction microscopy¹ has been used to image an entire freeze dried cell, unstained, using 750eV X-rays, with an image resolution of 30 nm². The method is currently being extended to hydrated and 3D samples. The extension of the work has several challenging areas including sample preparation and phase reconstruction.

For application to hydrated organic specimens such as in some soft condensed matter studies and especially for biological applications, it is essential to work with specimens in the frozen hydrated state at liquid nitrogen or lower temperature. For this reason we have built a specialized apparatus with a cryo specimen mount and airlock sample exchange mechanism³, and we are now working with an automated plunge-freezing system. With these improvements, we are beginning to collect tilt series x-ray diffraction data. We will discuss steps taken to improve ice thickness uniformity, frost reduction, and specimen pre-alignment, and present our current progress on x-ray diffraction imaging the yeast *Saccharomyces cerevisiae* carrying the *wi5* mutation, and the bacterium *Deinococcus radiodurans*. We will also discuss the effects of ice thickness variations on the compact support requirement of finite support iterative phase retrieval algorithms.

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